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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/711,619

DATE: 12/01/2000
TIME: 11:36:45

Input Set : A:\2054581.app
Output Set: N:\CRF3\12042000\I711619.raw

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      3 <110> APPLICANT: Johal, Gurmukh S
      4       Multani, Dilbag S
      6 <120> TITLE OF INVENTION: SORGHUM DWARFING GENES AND METHODS OF USE
      8 <130> FILE REFERENCE: 5718-100 (035718/205458)
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/711,619
C--> 11 <141> CURRENT FILING DATE: 2000-11-13
     13 <150> PRIOR APPLICATION NUMBER: 60/165,176
     14 <151> PRIOR FILING DATE: 1999-11-12
     16 <160> NUMBER OF SEQ ID NOS: 9
     18 <170> SOFTWARE: PatentIn Ver. 2.1
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     21 <211> LENGTH: 2139
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Sorghum bicolor
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     28 gtggccaacc tgcgcaccgt ggccgcgttc aacgcggagc gcaagatcac gggyctgttc 180
     29 gaggccaacc tgcgcgggcc gctccggcgc tgcttctgga agggggcagat cgccggcagc 240
     30 ggctacyggg tggcgcagtt ccrgctgtac gcgtcctacg cgctgggggt gtggtacgcg 300
     31 gcgtggctgg tgaagcacgg cgtgtccgac ttctcgcgca ccatccgcgt gttcatggtg 360
     32 ctgatggtgt ccgccaacgg cgccgccgag acgctgacgc tggcgccgga ctttgtcaag 120
     33 ggcggacgcg cgatgcggtc cgtgttcgag accatcgacc ggaaaacgga ggtggagccc 480
     34 gacgacgtgg acgcggcgcc ggtgccggag cggccaagg gcgaggtgga gctgaagcac 540
     35 gtggacttct cgtaccgtc gcggccggac atccaggtgt tccgcgacct gagcctccgg 600
     36 gcgcgcgccy ggaagacgct ggcgctggtg ggtccgagcg ggtgcyggca gagctcggtg 660
     37 ctggcgctgg cgcagcggtt ctacgagccc acgtccgggc gcgtgctcct ggacggcaag 720
     38 gacgtycgca agtacaacct gcgggcgctg cggcgcgtgg tggcggtggt gccgcaggag 780
     39 ccgttcctgt tcgcggcgag catccacgac aacatcgcgt acgggcgcga gggcgcgacg 840
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     42 cagcggatcg cgatcgcgcg cgcgctggtg aagcaagcgg gcatcatgcc gctggacgag 1020
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     45 cttgctgacg cgtcctacgc gcttggggtt ttggtaccgc gcgtggctag tgaagccacgg 1200
     46 gtctccgact ttcgcgcacc atccgggtgt tcatggtgct gatggtgtcc gccaacggcg 1260
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RAW SEQUENCE LISTING DATE: 12/04/2000
PATENT APPLICATION: US/09/711,619 TIME: 11:36:45

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Output Set: N:\CRF3\12042000\I711619.raw

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60 ggtggcggag cagggtcgc actcgcacct gctcaagcac catcccgacg ggtgctacgc 2100
61 gcggatgctg cagctgcagc ggctgacggg cgcggcggc                       2139
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65 <211> LENGTH: 1267
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67 <213> ORGANISM: Sorghum bicolor
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71 ggcttctcgg gggacctgga ggccgcgcac gccagggcca cgcagatcgc gggcgaggcc 120
72 gtggccaacc tgcgcaccgt ggccgcgttc aacgcggagc gcaaggatcac gggggctgtc 180
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74 ggctacgacg tggcgcagtt cctgctgtac gcgtcctacg cgctgggggt gtggtacgcg 300
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77 aggacgaggc cgcgatgcgg tcggtgttcg agacgatcga ccgcaagacg gaggtggagc 480
78 ccgacgacgt ggacgcggcg ccggtgccgg agcggccaag gaggcgaggtg gagctgaagc 540
79 acgtggactt ctcgtacccg tcgcggccgg acatccaggt gttccgcgac ctgagcctcc 600
80 gtgcgcgcgc cgggaagacg ctggcgctgg tgggccgag cgggtgcggc aagagctccgg 660
81 tgctggctct ggtgcagcgg ttctacaagc ccacgtccgg gcgcgtgttc ttgacggcaa 720
82 agacgtgcgc aaaacaacc ttcgggcgtt ccggcgcatt gttgcggtgg tacccaagaa 780
83 ccccgttcct gttcgcggcg aagaatccac gagaacatcg cgcacgggcg agagggcgct 840
84 acggaggcgg aggtggtgga ggcggcgccg caggcgaacg cgcaccgctt catcgcggcg 900
85 ctgccggaag gggtactgga cgcagaaggg cgagcgcggg gtgcacctgt cggggggcag 960
86 cggcagcgga tcgcgatcgc gcgcgcgctg gtgaagcagc ggccatcgtg ctgctggacg 1020
87 aggcgaccag cgcgctggac gccgagtcgg agcggtgcgt gcaggaggcg ctggagcgcg 1080
88 cgggtccgg gcgcaccacc atcgtggtgg cgcaccggct ggccacggtg cgcggcgcgc 1140
89 acaccatcgc ggtcatcgac gacggcaagg tggcggagca gggatcgcac tcgcacctgc 1200
90 tcaagcacca tccgacggg tgctacgcgc ggatgctgca gctgcagcgg ctgacgggcg 1260
91 cggcggc                                                        1267
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95 <211> LENGTH: 1261
96 <212> TYPE: DNA
97 <213> ORGANISM: Sorghum bicolor
99 <220> FEATURE:
100 <221> NAME/KEY: CDS
101 <222> LOCATION: (1)..(1245)
103 <400> SEQUENCE: 3
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106   1               5                  10                  15
108 atg ttc atg aag ggc ttc tcg ggg gac ctg gag gcc gcg cac gcc agg   96
109 Met Phe Met Lys Gly Phe Ser Gly Asp Leu Glu Ala Ala His Ala Arg
110             20                  25                  30
112 gcc acg cag atc gcg ggc gag gcc gtg gcc aac ctg cgc acc gtg gcc   144
113 Ala Thr Gln Ile Ala Gly Glu Ala Val Ala Asn Leu Arg Thr Val Ala
114         35                  40                  45
116 gcg ttc aac gcg gag cgc aag atc acg ggg ctg ttc gag gcc aac ctg   192
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PATENT APPLICATION: US/09/711,619

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117 Ala Phe Asn Ala Glu Arg Lys Ile Thr Gly Leu Phe Glu Ala Asn Leu
118      50                  55                  60
120 cgc ggc ccg ctc cgg cgc tgc ttc tgg aag ggg cag atc gcc ggc agc   240
121 Arg Gly Pro Leu Arg Arg Cys Phe Trp Lys Gly Gln Ile Ala Gly Ser
122  65                  70                  75                  80
124 ggc tac ggc gtg gcg cag ttc ctg ctg tac gcg tcc tac gcg ctg ggg   288
125 Gly Tyr Gly Val Ala Gln Phe Leu Leu Tyr Ala Ser Tyr Ala Leu Gly
126                  85                  90                  95
128 ctg tgg tac gcg gcg tgg ctg gtg aag cac ggc gtg tcc gac ttc tcg   336
129 Leu Trp Tyr Ala Ala Trp Leu Val Lys His Gly Val Ser Asp Phe Ser
130             100                 105                 110
132 cgc acc atc cgc gtg ttc atg gtg ctg atg gtg tcc gcc aac ggc gcc   384
133 Arg Thr Ile Arg Val Phe Met Val Leu Met Val Ser Ala Asn Gly Ala
134         115                 120                 125
136 gcc gag acg ctg acg ctg gcg ccg gac ttt gtc aag ggc ggg cgc gcg   432
137 Ala Glu Thr Leu Thr Leu Ala Pro Asp Phe Val Lys Gly Gly Arg Ala
138     130                 135                 140
140 atg cgg tcc gtg ttc gag acc atc gac cgg aaa acg gag gtg gag ccc   480
141 Met Arg Ser Val Phe Glu Thr Ile Asp Arg Lys Thr Glu Val Glu Pro
142 145                 150                 155                 160
144 gac gac gtg gac gcg gcg ccg gtg ccg gag cgg ccc aag ggc gag gtg   528
145 Asp Asp Val Asp Ala Ala Pro Val Pro Glu Arg Pro Lys Gly Glu Val
146                 165                 170                 175
148 gag ctg aag cac gtg gac ttc tcg tac ccg tcg cgg ccg gac atc cag   576
149 Glu Leu Lys His Val Asp Phe Ser Tyr Pro Ser Arg Pro Asp Ile Gln
150             180                 185                 190
152 gtg ttc cgc gac ctg agc ctc cgg gcg cgc gcc ggg aag acg ctg gcg   624
153 Val Phe Arg Asp Leu Ser Leu Arg Ala Arg Ala Gly Lys Thr Leu Ala
154         195                 200                 205
156 ctg gtg ggt ccg agc ggg tgc ggc aag agc tcg gtg ctg gcg ctg gtg   672
157 Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Ser Val Leu Ala Leu Val
158     210                 215                 220
160 cag cgg ttc tac gag ccc acg tcc ggg cgc gtg ctc ctg gac ggc aag   720
161 Gln Arg Phe Tyr Glu Pro Thr Ser Gly Arg Val Leu Leu Asp Gly Lys
162 225                 230                 235                 240
164 gac gtg cgc aag tac aac ctg cgg gcg ctg cgg cgc gtg gtg gcg gtg   768
165 Asp Val Arg Lys Tyr Asn Leu Arg Ala Leu Arg Arg Val Val Ala Val
166                 245                 250                 255
168 gcg ccg cag gag ccg ttc ctg ttc gcg gcg agc atc cac gac aac atc   816
169 Ala Pro Gln Glu Pro Phe Leu Phe Ala Ala Ser Ile His Asp Asn Ile
170             260                 265                 270
172 gcg tac ggg cgc gag ggc gcg acg gag gcg gag gtg gtg gag gcg gcg   864
173 Ala Tyr Gly Arg Glu Gly Ala Thr Glu Ala Glu Val Val Glu Ala Ala
174         275                 280                 285
176 acg cag gcg aac gcg cac cgg ttc atc gcg gcg ctg ccg gag ggc tac   912
177 Thr Gln Ala Asn Ala His Arg Phe Ile Ala Ala Leu Pro Glu Gly Tyr
178     290                 295                 300
180 ggg acg cag gtg ggc gag cgc ggg gtg  g ctg tcg ggc ggg cag cgg   960
181 Gly Thr Gln Val Gly Glu Arg Gly Val Gln Leu Ser Gly Gly Gln Arg
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182 305                 310                 315                 320
184 cag cgg atc gcg atc gcg cgc gct ggt aag cag cgg cca tcg tgc tgc   1008
185 Gln Arg Ile Ala Ile Ala Arg Ala Gly Lys Gln Arg Pro Ser Cys Cys
186                 325                 330                 335
188 tgg acg agg cga cca gcg cgc tgg acg ccg agt cgg agc ggt gcg tgc   1056
189 Trp Thr Arg Arg Pro Ala Arg Trp Thr Pro Ser Arg Ser Gly Ala Cys
190             340                 345                 350
192 agg agg cgc tgg agc gcg cgg ggt ccg ggc gca cca cca tcg tgg tgg   1104
193 Arg Arg Arg Trp Ser Ala Arg Gly Pro Gly Ala Pro Pro Ser Trp Trp
194         355                 360                 365
196 cgc acc ggc tgg cca cgg tgc gcg gcg cgc aca cca tcg cgg tca tcg   1152
197 Arg Thr Gly Trp Pro Arg Cys Ala Ala Arg Thr Pro Ser Arg Ser Ser
198     370                 375                 380
200 acg acg gca agg tgg cgg agc agg ggt cgc act cgc acc tgc tca agc   1200
201 Thr Thr Ala Arg Trp Arg Ser Arg Gly Arg Thr Arg Thr Cys Ser Ser
202 385                 390                 395                 400
204 acc atc ccg acg ggt gct acg cgc gga tgc tgc agc tgc agc ggc       1245
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206                 405                 410                 415
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214 <213> ORGANISM: Sorghum bicolor
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221             20                  25                  30
223 Ala Thr Gln Ile Ala Gly Glu Ala Val Ala Asn Leu Arg Thr Val Ala
224         35                  40                  45
226 Ala Phe Asn Ala Glu Arg Lys Ile Thr Gly Leu Phe Glu Ala Asn Leu
227     50                  55                  60
229 Arg Gly Pro Leu Arg Arg Cys Phe Trp Lys Gly Gln Ile Ala Gly Ser
230 65                  70                  75                  80
232 Gly Tyr Gly Val Ala Gln Phe Leu Leu Tyr Ala Ser Tyr Ala Leu Gly
233                 85                  90                  95
235 Leu Trp Tyr Ala Ala Trp Leu Val Lys His Gly Val Ser Asp Phe Ser
236             100                 105                 110
238 Arg Thr Ile Arg Val Phe Met Val Leu Met Val Ser Ala Asn Gly Ala
239         115                 120                 125
241 Ala Glu Thr Leu Thr Leu Ala Pro Asp Phe Val Lys Gly Gly Arg Ala
242     130                 135                 140
244 Met Arg Ser Val Phe Glu Thr Ile Asp Arg Lys Thr Glu Val Glu Pro
245 145                 150                 155                 160
247 Asp Asp Val Asp Ala Ala Pro Val Pro Glu Arg Pro Lys Gly Glu Val
248                 165                 170                 175
250 Glu Leu Lys His Val Asp Phe Ser Tyr Pro Ser Arg Pro Asp Ile Gln
251             180                 185                 190
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/711,619

DATE: 12/04/2000
TIME: 11:46:45

Input Set : A:\2054581.app
Output Set: N:\CRF3\12042000\I711619.raw

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254         195                 200                 205
256 Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Ser Val Leu Ala Leu Val
257     210                 215                 220
259 Gln Arg Phe Tyr Glu Pro Thr Ser Gly Arg Val Leu Leu Asp Gly Lys
260 225                 230                 235                 240
262 Asp Val Arg Lys Tyr Asn Leu Arg Ala Leu Arg Arg Val Val Ala Val
263                 245                 250                 255
265 Ala Pro Gln Glu Pro Phe Leu Phe Ala Ala Ser Ile His Asp Asn Ile
266             260                 265                 270
268 Ala Tyr Gly Arg Glu Gly Ala Thr Glu Ala Glu Val Val Glu Ala Ala
269         275                 280                 285
271 Thr Gln Ala Asn Ala His Arg Phe Ile Ala Ala Leu Pro Glu Gly Tyr
272     290                 295                 300
274 Gly Thr Gln Val Gly Glu Arg Gly Val Gln Leu Ser Gly Gly Gln Arg
275 305                 310                 315                 320
277 Gln Arg Ile Ala Ile Ala Arg Ala Gly Lys Gln Arg Pro Ser Cys Cys
278                 325                 330                 335
280 Trp Thr Arg Arg Pro Ala Arg Trp Thr Pro Ser Arg Ser Gly Ala Cys
281             340                 345                 350
283 Arg Arg Arg Trp Ser Ala Arg Gly Pro Gly Ala Pro Pro Ser Trp Trp
284         355                 360                 365
286 Arg Thr Gly Trp Pro Arg Cys Ala Ala Arg Thr Pro Ser Arg Ser Ser
287     370                 375                 380
289 Thr Thr Ala Arg Trp Arg Ser Arg Gly Arg Thr Arg Thr Cys Ser Ser
290 385                 390                 395                 400
292 Thr Ile Pro Thr Gly Ala Thr Arg Gly Cys Cys Ser Cys Ser Gly
293                 405                 410                 415
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298 <211> LENGTH: 26
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300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
304       primer designed from sequence of Zea mays Br2 gene
306 <400> SEQUENCE: 5
307 ctcctcgccg tgttcccgct cgtcgt                                          26
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311 <211> LENGTH: 17
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313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
317       primer designed from sequence of Zea mays Br2 gene
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323 <210> SEQ ID NO: 7
324 <211> LENGTH: 6827
325 <212> TYPE: DNA
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/711,619

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TIME: 11:36:46

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date